

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: GRAY, Joe W.
COLLINS, Colin
HWANG, Soo-In
GODFREY, Tony
KOWBEL, David
ROMMENS, Johanna

(ii) TITLE OF INVENTION: GENES FROM THE 20q13 AMPLICON AND THEIR USES

(iii) NUMBER OF SEQUENCES: 44

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Townsend and Townsend and Crew
(B) STREET: Two Embarcadero Center, 8th Floor
(C) CITY: San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94111-3834

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/731,499
(B) FILING DATE: 16-OCT-1996
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/680,395
(B) FILING DATE: 15-JUL-1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Hunter, Tom
(B) REGISTRATION NUMBER: 38,498
(C) REFERENCE/DOCKET NUMBER: 23070-068910

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (415) 576-0200
(B) TELEFAX: (415) 576-0300

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3000 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..3000
(D) OTHER INFORMATION: /note= "cDNA clone 3bf4 of 3kb transcript of tyrosine kinase gene A6"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCGCCGGCCG	GGCGCCTGG	CTGCACTCAG	CGCCGGAGCC	GGGAGCTAGC	GGCCGCCGCC	60
ATGTCCCACC	AGACCGGCAT	CCAAGCAAGT	GAAGATGTTA	AAGAGATCTT	TGCCAGAGCC	120
AGAAATGGAA	AGTACAGACT	TCTGAAAATA	TCTATTGAAA	ATGAGCAACT	TGTGATTGGA	180
TCATATAGTC	AGCCTTCAGA	TTCCTGGAT	AAGGATTATG	ATTCCCTTGT	TTTACCCCTG	240
TTGGAGGACA	AACAACCATG	CTATATATTA	TTCAGGTTAG	ATTCTCAGAA	TGCCCAGGGA	300
TATGAATGGA	TATTCAATTGC	ATGGTCTCCA	GATCATTCTC	ATGTTCGTCA	AAAAATGTTG	360
TATGCAGCAA	CAAGAGCAAC	TCTGAAGAAG	GAATTGGAG	GTGCCACAT	TAAAGATGAA	420
GTATTTGGAA	CAGTAAAGGA	AGATGTATCA	TTACATGGAT	ATAAAAAATA	CTTGCTGTCA	480
CAATCTTCCC	CTGCCCACT	GACTGCAGCT	GAGGAAGAAC	TACGACAGAT	AAAAATCAAT	540
GAGGTACAGA	CTGACGTGGG	TGTGGACACT	AAGCATCAAA	CACTACAAGG	AGTAGCATT	600
CCCATTTCTC	GAGAACGCTT	TCAGGCTTG	AAAAAATTGA	ATAATAGACA	GCTCAACTAT	660
GTGCAGTTGG	AAATAGATAT	AAAAAATGAA	ATTATAATT	TGGCCAACAC	AACAAATACA	720
GAAC TGAAAG	ATTTGCCAAA	GAGGATTCCC	AAGGATTCA	CTCGTTACCA	TTTCTTCTG	780
TATAAACATT	CCCATGAAGG	AGACTATT	GAGTCATAG	TTTTTATT	TTCAATGCCT	840
GGATACACAT	GCAGTATAAG	AGAGCGGATG	CTGTATTCTA	GCTGCAAGAG	CCGTCTGCTA	900
GAAATTGTAG	AAAGACAAC	ACAAATGGAT	GTAATTAGAA	AGATCGAGAT	AGACAATGGG	960
GATGAGTTGA	CTGCAGACTT	CCTTTATGAA	GAAGTACATC	CCAAGCAGCA	TGCACACAA	1020
CAAAGTTTG	CAAAACAAA	AGGTCCCTGCA	GGAAAAAGAG	GAATTGAG	ACTAATTAGG	1080
GGCCCAGCGG	AAACTGAAGC	TACTACTGAT	TAAAGTCATC	ACATTAAACA	TTGTAATACT	1140
AGTTTTTAA	AACTCCAGCT	TTTAGTACAG	GAGAACTGAA	ATCATTCCAT	GTTGATATAA	1200
AGTAGGGAAA	AAAATTGTAC	TTTTGGAAA	ATAGCACTT	TCACTTCTGT	GTGTTTTAA	1260
AATTAATGTT	ATAGAAGACT	CATGATTCT	ATTTTGAGT	TAAAGCTAGA	AAAGGGTTCA	1320
ACATAATGTT	TAATTTGTC	ACACTGTTT	CATAGCGTTG	ATTCCACACT	TCAAATACTT	1380
CTTAAAATT	TATACAGTTG	GGCCAGTTCT	AGAAAGTCTG	ATGTCTAAA	GGGTAAACTT	1440
ACTACTTCT	TGTGGGACAG	AAAGACCTTA	AAATATTCA	ATTACTTAAT	GAATATGTTA	1500
AGGACCAGGC	TAGAGTATT	TCTAAGCTGG	AAACTTAGTG	TGCCTTGAA	AAGCCGCAAG	1560
TTGCTTACTC	CGAGTAGCTG	TGCTAGCTCT	GTCAGACTGT	AGGATCATGT	CTGCAACTTT	1620
TAGAAATAGT	GCTTATATT	GCAGCAGTCT	TTTATATTG	ACTTTTTTT	AATAGCATTA	1680
AAATTGCAGA	TCAGCTCACT	CTGAAAC	AAGGGTACCA	GATATTCT	ATACTGCAGG	1740
ATTTCTGATG	ACATTGAAAG	ACTTTAAACA	GCCTTAGTAA	ATTATCTTC	TAATGCTCTG	1800
TGAGGCCAAA	CATTATGTT	CAGATTGAAA	TTTAAATTAA	TATCATTCAA	AAGGAAACAA	1860
AAAATGTTGA	GTTTAAAAAA	TCAGGATTGA	CTTTTTCTC	CAAACCCATA	CATTTATGGG	1920
CAAATTGTTGT	TCTTATCAC	TTCCGAGCAA	ATACTCAGAT	TTAAAATTAC	TTTAAAGTCC	1980

TGGTACTTAA CAGGCTAACG TAGATAAACCA CCTTAATAAT CTCAGTTAAT ACTGTATTC	2040
AAAACACATT TAACTGTTT CTAATGCTTT GCATTATCAG TTACAAACCTA GAGAGATTT	2100
GAGCCTCATA TTTCTTGAT ACTTGAAATA GAGGGAGCTA GAACACTTAA TGTTTAATCT	2160
GTAAACCTG CTGCAAGAGC CATAACTTG AGGCATTTTC TAAATGAAC GTGGGGATCC	2220
AGGATTTGTA ATTTCTTGAT CTAAACTTAA TGCTGCATAA ATCACTTATC GGAAATGCAC	2280
ATTTCATAGT GTGAAGCACT CATTCTAAA CCTTATTATC TAAGGTAATA TATGCACCTT	2340
TCAGAAATTG GTGTCGAGT AAGTAAAGCA TATTAGAATA ATTGTGGTT GACAGATTT	2400
TAAAATAGAA TTTAGAGTAT TTGGGTTTT GTTGTAC AAATAATCAG ACTATAATAT	2460
TTAACATGC AAAATAACTG ACAATAATGT TGCACTTGTT TACTAAAGAT ATAAGTTGTT	2520
CCATGGGTGT ACACGTAGAC AGACACACAT ACACCCAAAT TATTGCATTA AGAACCTGG	2580
AGCAGACCAT AGCTGAAGCT GTTATTTCA GTCAGGAAGA CTACCTGTCA TGAAGGTATA	2640
AAATAATTAA GAAGTGAATG TTTTCTGTA CCATCTATGT GCAATTATAC TCTAAATTCC	2700
ACTACACTAC ATTAAAGTAA ATGGACATTC CAGAATATAG ATGTGATTAT AGCTTAAAC	2760
TAATTATTAT TAAACCAATG ATTGCTGAAA ATCAGTGATG CATTGTTAT AGAGTATAAC	2820
TCATCGTTA CAGTATGTT TAGTTGGCAG TATCATACT AGATGGTAA TAACATATTCA	2880
CCAGTAAATT TATATAGCAG TGAAGAATTA CATGCCTTCT GGTGGACATT TTATAAGTGC	2940
ATTTTATATC ACAATAAAAAA TTTTTCTCT TTAAAAAAA AAAACAAGAA AAAAAAAAAA	3000

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 723 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..723
- (D) OTHER INFORMATION: /note= "cDNA clone 1b11 of 3.5kb transcript"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TGGAAGCTGT CATGGTTACC GTCTCTAACG TTGGACTCTT AAGAAAATGA TTATTCCTGG	60
TTTCTAGACA GGCCAAATGT AATTCACTTA CGTGGCAGAT TAAAGAGGTG GGCTTACTAG	120
ATTTGATTGG GTATTGAGCA TGCTCTGAAT GACAGTCCCC AAAAAGGACC TCTTATCCGT	180
TCTTCCCCCTT GGGGAAGGGC TTTTGCCACT TCCATGTCAA TGTGGCAGTT GAGCTTGGAA	240
ATTGGTGCCT TGTACAACAT AAGCATTACT TCTCCAAGAT GTGCCTGTGT AGAAATGGTC	300
ATAGATTCAA AACTGTAGCT ACTATGTGGA CAGGGGGCA GCAAGGACCC CACTTTGTAA	360

AACATGTTT GGGGAATGT TTTGTTTTC ATTTCTTAT TACCTGGCAA AATAATCCAG	420
GTGGTGTGTG AGTCACCACT AGAGATTATA AAGTCCAAGG AAGTACAATC AGCCTTACAA	480
ACAGTGGACC TCAACGAAGG AGATGCTGCA CCTGAACCCA CWGAAGCGAA ACTCAAAAGA	540
GAAGAAAGCA AACCAAGAAC CTCTCTGATG RCGTTCTCA GACAAATGGT AAGCCCCTTA	600
CTTCCAGTAT AGGAAACCTA AGATACCTAG AGCGGTTTT GGGAAACAATG GGCTCATGCC	660
ACAGGTAGTA GGAGACATAA TTGTAGCTGG TGTGTATGGA ATGTGAATGG AATATGGATT	720
GCG	723

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1507 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1507
- (D) OTHER INFORMATION: /note= "cDNA clone cc49 of 6-7kb transcript with homology to C2H2 zinc finger genes"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCAGGTTGCT GGGATTGACT TCTTGCTCAA TTGAAACACT CATTCAATGG AGACAAAGAG	60
CACTAATGCT TTGTGCTGAT TCATATTGAT ATCGAGGCAT TGGGAACCCCT GTATGCCTTG	120
TTTGTGGAAA GAACCACTGAA CACCATCACT GAGCTTCCTA AAAGTTGAA GAAGTTAGAG	180
GACTATACAC TTTCTTTGAA ACTTTTATAA TAAATATTTG CTCTGGTTTT GGAACCCAGG	240
ACTGTTAGAG GGTGAGTGAC AGGTCTTACA GTGGCCTTAA TCCAACCTCA GAAATTGCC	300
AACGGAACCTT TGAGATTATA TGCAATCGAA AGTACAGAGGA AACATGCCAA CTCAATCCCT	360
CTTAATGTAC ATGGATGGCC AAGAGTGATT GGCAGCTCTC TTGCCAGTCC GATGGAGATG	420
GAGATGCCTT GTCAATGAAA GGGCCCNCTG TTGTCAATTG CGAGCTACAC AAAGAAAAAA	480
ATGTCAATCC GAATCGAGGG GAATATGCC TTGGATTGCA TGTTCTGCAG CCAGACCTTC	540
ACACATTCAAG AAGACCTTAA TAAACATGTC TTAATGCAAC ACCGGCCTAC CCTCTGTGAA	600
CCAGCAGTTC TTCGGGTTGA AGCAGAGTAT CTCAGTCCGC TTGATAAAAG TCAAGTGCAG	660
ACAGAACCTC CCAAGGAAAA GAATTGCAAG GAAAATGAAT TTAGCTGTGA GGTATGTGGG	720
CAGACATTAA GAGTCGCTTT TGATGTTGAG ATCCACATGA GAACACACAA AGATTCTTC	780
ACTTACGGGT GTAACATGTG CGGAAGAAGA TTCAAGGAGC CTTGGTTCT TAAAAATCAC	840
ATGCGGACRC ATAATGGCAA ATCGGGGCC AGAAGCAAAC TGCAGCAAGG CTTGGAGAGT	900
AGTCCAGCAA CGATCAACGA GGTGCGCCAG GTGCACGCGG CCGAGAGCAT CTCCCTCTCCT	960

TGCAAAATCT GCATGGTTG TGGCTTCCTA TTTCCAAATA AAGAAAGTCT AATTGAGCAC	1020
CGCAAGGTGC ACACCAAAAA AACTGCTTTC GGTACCAGCA GCGCGCAGAC AGACTCTCCA	1080
CAAGGAGGAA TGCCGTCCTC GAGGGAGGAC TTCCTGCAGT TGTTCAACTT GAGACCAAAA	1140
TCTCACCCCTG AAACGGGGAA GAAGCCTGTC AGATGCATCC CTCAGCTCGA TCCGTTCAC	1200
ACCTTCCAGG CTTGGCAKCT GGCTACCAAA GGAAWAGTTG CCATTTGCCA AGAAGTGAAG	1260
GAATTGGGC AAGAAGGGAG CACCGACAAC GACGATTCGA GTTCCGAGAA GGAGCTTGG	1320
GAAACAAATA AGAACCATTG TGCAGGCCTC TCGCAAGAGA AAGAGAAGTG CAAACACTCC	1380
CACGGCGAAG CGCCCTCCGT GGACGCGGAT CCCAAGTTAC CCAGTAGCAA GGAGAAGCCC	1440
ACTCACTGCT CCGAGTGCAG CAAAGCTTTC AGAACCTACC ACCAGCTGGT CTTGCACTCC	1500
AGGGTCC	1507

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2605 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..2605
- (D) OTHER INFORMATION: /note= "cDNA clone cc43 of 4 kb transcript"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CAAGCTCGAA ATTAACCCCTC ACTAAAGGGA ACAAAAGCTG GAGCTCCACC GCGGTGGCGG	60
CCGCTCTAGA ACTAGTGGAT CCCCCGGGCT GCAGGAATTC GGCACGAGCT GGGCTACTAC	120
GATGGCGATG AGTTTCGAGT GGCGTGGCA GTATCGCTTC CCACCCCTCT TTACGTTACA	180
ACCGAATGTG GACACTCGGC AGAAGCAGCT GGCCGCCTGG TGCTCGCTGG TCCTGTCC	240
CTGCCGCCTG CACAAACAGT CCAGCATGAC GGTGATGGAA GCTCAGGAGA GCCCGCTCTT	300
CAACAAACGTC AAGCTACAGC GAAAGCTTCC TGTGGAGTCG ATCCAGATTG TATTAGAGGA	360
ACTGAGGAAG AAAGGGAACC TCGAGTGGTT GGATAAGAGC AAGTCCAGCT TCCTGATCAT	420
GTGGCGGAGG CCAGAAGAAT GGGGGAAACT CATCTATCAG TGGGTTCCA GGAGTGGCCA	480
GAACAACTCC GTCTTACCC TGTATGAAC GACTAATGGG GAAGACACAG AGGATGAGGA	540
GTTCCACGGG CTGGATGAAG CCACTCTACT GCGGGCTCTG CAGGCCCTAC AGCAGGAGCA	600
CAAGGCCGAG ATCATCACTG TCAGCGATGG CCGAGGCGTC AAGTTCTTCT AGCAGGGACC	660
TGTCTCCCTT TACTTCTTAC CTCCCACCTT TCCAGGGCTT TCAAAAGGAG ACAGACCCAG	720
TGTCCCCCAA AGACTGGATC TGTGACTCCA CCAGACTCAA AAGGACTCCA GTCCTGAAGG	780

CTGGGACCTG	GGGATGGGTT	TCTCACACCC	CATATGTCTG	TCCCTGGAT	AGGGTGAGGC	840
TGAAGCACCA	GGGAGAAAAT	ATGTGCTTCT	TCTCGCCCTA	CCTCCTTCC	CATCCTAGAC	900
TGTCCCTGAG	CCAGGGTCTG	TAAACCTGAC	ACTTTATATG	TGTTCACACA	TGTAAGTACA	960
TACACACATG	CGCCTGCAGC	ACATGCTTCT	GTCTCCTCCT	CCTCCCACCC	CTTTAGCTGC	1020
TGTTGCCTCC	CTTCTCAGGC	TGGTGCTGGA	TCCTTCCTAG	GGGATGGGGG	AAGCCCTGGC	1080
TGCAGGCAGC	CTTCCAGGCA	ATATGAAGAT	AGGAGGCCA	CGGGCCTGGC	AGTGAGAGGT	1140
GTGGCCCCAC	ACCGATTAT	GATATTTAA	TCTCAACTCC	CAAAAAAAA	AAAAAAA	1200
CTGAGACTAG	TTCTCTCT	CTCGAGAACT	AGTCTCGAGT	TTTTTTTTT	TTTTTTTTT	1260
TTTTTTTTT	TTTTTTTTG	GCTTTAAGGA	TTTATTTATT	GTTTCCTCTT	TACAGTGTCC	1320
ACTTTCTCT	ACTTAATACT	ACTTTCCAGT	CTCAGAAGCC	CAGAGGGAAA	AAAAAAAGAC	1380
CATGAATCTT	CCTCTCCCAG	ATTAAAGTAC	ACACTTTGGA	AAACAGATTG	GAAAACCTTT	1440
CTGAAAAAAAG	TTGACTGAAA	CTCCAAACCA	ACATGCCATA	TTGTTGATGT	TGCTCATGAA	1500
AATTGTTAAA	AACCTGTTCT	AGATAAAGAA	CAGTCTCAAG	TTTTTGATCA	GCCTACACAT	1560
AGTACAAGGG	TCCCCTATGA	TGATTCTTCT	GTAGGACGAA	ATAATGTAAT	TTTTTCAGTT	1620
TCTGGTTTAT	AACTCTCTCG	ATCTCAGAGT	TGACTGATTA	AAACACCTAC	TCATGCAACA	1680
GAGAATAAAG	CACTCATATT	TTTATAAATT	ATATGGACCA	AACTATTTG	GAAATCTTAT	1740
CTATTGGAGA	CACAATATGC	TGGACTAAAG	CAATAATTAT	TTTATTCTCA	ATGTCTGTGC	1800
TAACCTCAAT	GACTAGAAT	GCTTGCTAT	ATTTGCCTC	TATGCCTCAA	CCACACTGGC	1860
TTTCTTTAG	CTCTGAACA	AGCCAAACTG	CTTCCTGCCT	CAGGACCAGA	TATTTGGGA	1920
CTTCTCTTAA	GAATTCTATT	TCCTTAATTC	TTTATCTGGG	TAACCTAGTT	TTATCCAACA	1980
CTTCAGATCC	TGCCGTAAAA	ACTCTCTTA	TAGAAGCCTG	TCATGACACT	GTCTCTCTTC	2040
TCCAACATAC	TCACCAGCAC	ACATGTAGAC	TAGATTAGAA	CCTCCTGTTT	TTCTTTTCA	2100
TACTTTCTC	TATCATGCTT	CCCTCCATTA	TAATATTTT	ATTATGTGTG	TGAATGTCTG	2160
CCCCAAGTCA	GTTCCTCAC	TAAACTATAA	ACTCCGTAAA	GCTGGGATCC	TTCCAATT	2220
GATCACCAC	TAGTACAGTA	GGAACACAGT	AAAGATTCAA	TTGGTATTG	TGGAATGAAT	2280
GAATGAATTG	TTTGCTAGT	AAAGTCTGGG	GGAACCCAGG	TGAGAAGAGC	CTAGAAAGCA	2340
GGTCGAATCC	AAGGCTAGAT	AGACTTAGTG	TTACTCAAGA	AAGGGTAGCC	TGAAAATAAA	2400
GGTCAAATT	ATAGTCAAGA	ATAGTCAAGA	CATGGGCAAG	ACAAGAGTGC	TGCTCGTGC	2460
GAATTGATA	TCAAGCTTAT	CGATACCGTC	GACCTCGAGG	GGGGGCCCGG	TACCCAATT	2520
GCCCTATAGT	GAGTCGTATT	ACAATTCACT	GGCCGTCGTT	TTACAAACGTC	GTGACTGGGA	2580
AAACCCTGGC	GTTACCCAAC	TTAAT				2605

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1288 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1288
- (D) OTHER INFORMATION: /note= "cDNA clone 41.1 with homology to homeobox T shirt gene from Drosophila"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAGGGCAGCG AGAAGGAGAA ACCCCAGCCC CTGGAGCCCA CATCTGCTCT GAGCAATGGG	60
TGCGCCCTCG CCAACCACGC CCCGGCCCTG CCATGCATCA ACCCACTCAG CGCCCTGCAG	120
TCCGTCTGAA ACAATCACTT GGGCAAAGCC ACGGAGCCCT TGCGCTCACC TTCCCTGCTCC	180
AGCCCAAGTT CAAGCACAAT TTCCATGTTCA CACAAGTCGA ATCTCAATGT CATGGACAAG	240
CCGGTCTTGA GTCCTGCCTC CACAAGGTCA GCCAGCGTGT CCAGGCGCTA CCTGTTTGAG	300
AACAGCGATC AGCCCATTGA CCTGACCAAG TCCAAAAGCA AGAAAGCCGA GTCCCTCGCAA	360
GCACAATCTT GTATGTCCCC ACCTCAGAAG CACCGCTCTGT CTGACATCGC CGACATGGTC	420
AAAGTCCTCC CCAAAGCCAC CACCCCAAAG CCAGCCTCCT CCTCCAGGGT CCCCCCCCATG	480
AAGCTGGAAA TGGATGTCAG GCGCTTGAG GATGTCTCCA GTGAAGTCTC AACTTTGCAT	540
AAAAGAAAAG GCCGGCAGTC CAACTGGAAT CCTCAGCATC TTCTGATTCT ACAAGCCCAG	600
TTTGCCTCGA GCCTCTTCCA GACATCAGAG GGCAAATACC TGCTGTCTGA TCTGGGCCA	660
CAAGAGCGTA TGCAAATCTC TAAGTTACG GGACTCTCAA TGACCACTAT CAGTCACTGG	720
CTGGCCAACG TCAAGTACCA GCTTAGGAAA ACGGGCGGGA CAAAATTCT GAAAAACATG	780
GACAAAGGCC ACCCCATCTT TTATTGCAGT GACTGTGCCT CCCAGTTCA GACCCCTTCT	840
ACCTACATCA GTCACTTAGA ATCTCACCTG GGTTTCCAAA TGAAGGACAT GACCCGCTT	900
TCAGTGGACC AGCAAAGCAA GGTGGAGCAA GAGATCTCCC GGGTATCGTC GGCTCAGAGG	960
TCTCCAGAAA CAATAGCTGC CGAAGAGGAC ACAGACTCTA ATTCAAGTG TAAGTTGTGC	1020
TGTCGGACAT TTGTGAGCAA ACATGCGGTA AAACTCCACC TAAGCAAAAC GCACAGCAAG	1080
TCACCCGAAC ACCATTCACA GTTTGTAACA GACGTGGATG AAGAATAGCT CTGCAGGACG	1140
AATGCCTTAG TTTCCACTTT CCAGCCTGGA TCCCCTCACA CTGAACCTT CTTCGTTGCA	1200
CCATCCTGCT TCTGACATTG AACTCATTGA ACTCCTCCTG ACACCCCTGGC TCTGAGAAGA	1260
CTGCCAAAAAA AAAAAAAA AAAAATTC	1288

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2821 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: -
 (B) LOCATION: 1..2821
 (D) OTHER INFORMATION: /note= "cDNA clone GCAP encodes a guanino cyclase activating protein (GCAP)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATCCTAAGAC	GCACAGCCTG	GGAAGCCAGC	ACTGGGGAAG	TGGTGCTGAG	GGATGTGGGT	60
CACTGGGTG	AAGGTGGAGC	TTTCAGGGTC	TCCCGTCAAT	GCAGCTGAGT	TTTCTTTGGC	120
AGGAATTAA	CCAGCTGAAG	AAAGCCTGCC	GGCGAGAGCT	ACAAACTGAG	CAAGGCCAGC	180
TGCTCACACC	CGAGGAGGTC	GTGGACAGGA	TCTTCCTCCT	GGTGGATGAG	AATGGAGATG	240
GTAAGAGGGG	CAGAGATGGG	GAGAGTGCTG	TCCACTCTGC	ATCATCGCCA	CTTTCTGGCC	300
GCACGTCCTT	GGGCAAGGCC	CTCCACCTTC	CAACCCTGGG	GTCCTCATCT	GTGAGAAGGC	360
TGTGGAGAAG	ATGTCATGAA	CTAACAAAGG	GACTCATGAG	CACGTGTTG	TAGGAGTGAC	420
TAAAAGTCCT	ACAGGAGTTG	CTGATGGAGG	CCAGGCACGC	AGAATAGAAA	GAATAGGAAC	480
TTTGGAGTCA	GGCAGGGAGT	GATATATTGA	GCTTCTCGTC	CTAGTCTCAA	TTTCCTCATC	540
TGGAAAATGG	GGATAATAAT	AGTGGTTGAG	AGGAATGAAT	AGGATAATGT	TTTTAAGAGC	600
AGGCATAGGG	TAGACCTCCA	TTCAGGCTGC	TTGGGCTTTC	CTCCCTGTAG	CCCAAAGCCC	660
AGCCTCAGGG	CTATGTGGGG	AGAGAGCTGG	CTTGAATAC	ACACTTGAGC	CCTCCAGCTC	720
TCTCAGCTCC	ACCCAGCATT	TCCGTGGTAC	CATGCGAAA	AGTAAAACCTT	CAATTCATCA	780
GCAAAGAAAG	CCCCTTAAAG	GTGGCAGGAG	ACTCCTGGAG	ATTCAAGACAC	CTGACAAGCC	840
GCAAGCTTGA	GGTCTGAGAC	TGCAGGATAG	TTGGCATAAG	ACGTGTAGGC	GCATCCTGGG	900
AGCGAGGTCT	CTCCTCCTGC	CCCCAGACCC	AGGTCTCCCC	TTCTTCTACA	TGACCACCTC	960
TCCTCCCCCT	TGCTCAGGCC	AGCTGTCTCT	GAACGAGTTT	GTTGAAGGTG	CCCGTCGGGA	1020
CAAGTGGGTG	ATGAAGATGC	TGCAGATGGA	CATGAATCCC	AGCAGCTGGC	TCGCTCAGCA	1080
GAGACGGAAA	AGTGCCATGT	TCTGAGGAGT	CTGGGGCCCC	TCCACGACTC	CAGGCTCACC	1140
CAGGTTTCCA	GGGTAGTAGG	AGGGTCCCC	GGCTCAGCCT	GCTCATGCC	ACTCTTCCCC	1200
TGGTGTGAC	TTCTGGCAC	CCCCTGTGCA	GGGCTGAGTG	GGGATGGGGA	AGGGCTGCTG	1260
GGTTTGAAGT	GGCCAACAGG	GCATAGTCCA	TTTGGAGGA	GTCCCTGGGA	TGGTGAAGGG	1320
AATTCAAGTTA	CTTTCTGTGT	TCAGCCGCTC	CTGGGAGGAC	TGTGCCTTGG	CTGGGTGGTT	1380
GTGGGGCTCC	CACAGTTCT	GGGTGTTCTC	AGTTGGAAGC	AAGAGCCAAC	TGAGGGGTGA	1440
GGGTCCCACA	GACCAAATCA	GAAATGAGAA	CACAAAGACT	GGTAGGAGGC	AGGGGTGGGA	1500
GGGTGTTGAG	ACTGAAGAAA	AGGCAGGAGT	TGCCGGGCAC	GGTGGCTCAC	GCCTGTAATC	1560

CCAGCACTTT	GGGAGGGCCGA	GGCGGGCAGA	TCACGAGGTC	AGGAGATCGA	GACCATCCTG	1620
GCTAACACGG	GGTGAACACCC	CGTCTCTACT	AAAAATACAA	AAAATCAGCC	GGGTGAGGTG	1680
GCGGGCGCCT	GTAGTCCCAG	CTACTCAGGA	GGCTGAGGCA	AGAGAATGGC	GTGAACCCCA	1740
GGGGGCCGAG	CCTACAGTGA	GCCGAGATTG	CGCCACTGCA	CTCCAGCCTG	GACGACAGTG	1800
AGACTCCGTC	TCAAAAAAAA	AAAAAGAAAG	AAAAGAAAAG	GCAGGAGTTT	TGGGGGGCAG	1860
GGGGCAGCAA	TAATTCTATA	ACTTCCGGGA	TGCTGAGGGG	CGTTCATGGG	GAGGACCCCTG	1920
GCCTCCCTCT	CCCCAAGGCA	TCCTCACCAAG	TGGTGTCAAC	AGGAAAAATG	GCAGCAAATA	1980
CGCTGCAGGC	TGTGGTCTTT	CTGCCTTGA	AAGGGTCAGC	TGTACTTAAA	GGGACTGTTT	2040
CAGCTCTGCC	TGGGTGCTGC	TCTGGGACCC	CCTGCTGCCA	ACCCACCACT	CCCCCAACAA	2100
TCCTCTCTTT	CCATCCATAT	CCCCCAGTAT	GGACCTTCCA	CAACTCCCAG	CCATAAGCTG	2160
AATGTTTCTC	TTTAAAGGAT	GGAGAAAACT	TCTGTCTGTC	TCTGGCAAGA	ATTGGGGGAC	2220
TGTTGACTGG	GATTGTGGC	TGGGCTTGGC	TTCTAAGTGC	TGTGTGACCC	AAGACAGCCA	2280
CTTCTCCTCC	CTAACCTTGG	TTATGTCTTG	GCAGCACAGT	GAGCAGGTCG	GACTAGGCGA	2340
ACAGTTTTGG	ATTATTGTGT	TTTTAGATGT	GGAATTATTT	TTTGTATAT	AAACTCTTAT	2400
GTGTAACCCC	AATATAGAAA	CTAGATTAAA	AGGGAGTCTC	TCTGGTTGAA	AGGGGAGCTG	2460
AGTACCCCTCT	GGAACTGGAG	GCACCTCTGA	AAAAAGCAAA	CTGAAAACCA	GTGCCCTGGG	2520
TCACTGTTAC	TCCTATAAGA	CAGTTAAAG	TGAGACCTGG	AAAAACATTT	GCTTTACCTT	2580
GAATAGATAG	GTTTTTATGT	TGGTATATAA	GAAATAAAAC	TAACCTATTA	ACCCTGAGAC	2640
TTTACAGGTG	TGTTATTTCA	TATGATAGTC	ATATAAAATT	TCCTTAGAC	ATCAATTAA	2700
GGTAAAAAAAT	AATTGATTAG	AAAAATATTG	GCCAGGTGCA	GCAGCTCACA	CCTGCAATCC	2760
CAGGACTTTG	GGAGGCCGAG	GCAGGTGGAT	CACCTGAGGT	CAGGGTTCA	AGACCAGCCT	2820
G						2821

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1205 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..1205
 - (D) OTHER INFORMATION: /note= "cDNA clone 1b4 for a serine threonine kinase"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCGCGCGTGA GTCCGCCCGCC CCAGTCACGT GACCGCTGAC TCGGGCGTT CTCCACTATC

60

GCTTACCTAC	CTCCCTCTGC	AGGAACCCGG	CGATATGGCT	GCCGCTGTGC	CCCGCGCCGC	120
ATTTCCTCTCC	CCGCTGCTTC	CCTTCTCCTG	GGCTTCCTGC	TCCTCTCCGC	TCCGCATGGC	180
GGCAGCGGCC	TGCACACCAA	GGCGCCCTTC	CCCTGGATAC	GGTCACTTTC	TACAAGGTCA	240
TTCCCAAAAG	CAAGTCGTC	TGGTGAAGTT	CGACACCCAG	TACCCCTACG	GTGAGAAGCA	300
GGATGAGTTC	AAGCGTCTTC	TGAAAACCTCG	GCTCCAGCG	ATGATCTCTT	GGTGGCAGAG	360
GTGGGGATCT	CAGATTATGT	GACAAGCTGA	ACATGGAGCT	GAGTGAGAAA	TACAAGCTGG	420
ACAAAGAGAG	CTACCCATCT	TCTACCTCTT	CCGGGATGGG	GACTTGAGA	ACCCAGTCCC	480
ATACACTGGG	GCAGTTAGGT	TGGAGCCATC	CAGCGCTGGC	TGAAGGGGCA	AGGGGTCTAC	540
CTAGGTATGC	CTGGTGCCTG	CCTGTATACT	ACGCCCTGGC	CGGGGAGTTC	ATCAGGGCCT	600
CTGGTGTGGA	GGCCGCCAGG	CCCTCTTGAA	GCAGGGGCAA	GATAACCTCT	CAAGTGTGAA	660
GGAGACTCAG	AAGAGTGGC	CGAGCAATAC	CTGAAGATCA	TGGGAAAGAT	CTTAGACCAA	720
GGGGAGCACT	TCCAGCATCA	GAGATGACAC	GGATGCCAG	GCTGATTGAG	AAGAACAAAGA	780
TGAGTGACGG	CAGAAGGAGG	AGCTCCAGAA	GAGCTTAAAC	ATCCTGACTG	CCTTCCAGAA	840
GAAGGGGGCC	GAGAAAGAGG	AGCTGTAAAA	AGGCTGTCTG	TGATTTCCA	GGGTTTGGTG	900
GGGGTAGGGA	GGGGANAGTT	AACCTGCTGG	CTGTGANTCC	CTTGTGGAAT	ATAAGGGGGY	960
MSKGGGAAAA	GWGGTACTAA	CCCACGATT	TGAGCCCTGA	GTATGCCCTGG	ACATTGATGC	1020
TAACATGACC	ATGCTTGGGA	TGTCTCTAGC	TGGTCTGGGG	ATAGCTGGAG	CACTTACTCA	1080
GGTGGCTGGT	GAAATGACAC	CTCAGAAGGA	ATGAGTGCTA	TAGAGAGGAG	AGAGGAGTGT	1140
ACTGCCAGG	TCTTGACAG	ATGTAATTCT	CATTCAATT	AAGTTTCAGT	TTTTGGTTA	1200
AGTGG						1205

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..455
- (D) OTHER INFORMATION: /note= "cDNA clone 20sa7 for a homolog of rat gene BEM-1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GAAATCAGAA	GTTAATATG	ACACAATTAA	ATATATTGT	ATATCTCACA	CCGGAGNTTC	60
TCTTCAAACA	TAAGGAGTTA	GAAATTACAA	GTAAGCATAT	GCTTCCTATA	TTCAGATAAA	120
TTCATTTCGA	TTAATTAAAT	TCCAGATAGA	GAGAAGTAAT	TTTCGGAAAA	GAAATGATAG	180

CTATATTAAA GCAGATATTC ATTACAATAC CATGTAGAGA CATAAGCAAT ATTTTGGCAT	240
CATTCTGTCC GCTCAGTAGG CCGTGTCCC TCTGGTAGGG CCTTTGGAGA GTACCATCTA	300
TCTAAGATGG AGGAATGCTG TGGGAAGGGC GGGATGGAGG TGCGTTTCT ACGCTGAACC	360
CCACACAGGA AATCTGCAGC CCACACAGCT GCCTCTGCGC CGCCTTCCAT GTGATCATCC	420
TGGTCAATGA AGTGAATTGT CCTATTCNG GGGGT	455

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10365 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..10365
- (D) OTHER INFORMATION: /note= "Genomic Sequence Encoding ZABC1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CCATCATATT TCTTATTTTT TTGGCGGAG AGGGGAGACT TGCTCTGTTG CCCAGGCTGG	60
ACCACTGGTG CGATCTTGGC TCACTGCAAC CTCCACCTCC TGGGTTCAAG TGATTCCAA	120
ATAGCTGGGA TTACAGGTGT GTATTACCAT GCCCAGCTAA TTTTTGTATT TTTAGCAGAT	180
AAGGGGTTTC ACCATGTTGG CCAGGCTGGT CTCCAACCTCC TGGCCTCATG TGATCCACCC	240
ACTTCGGCTT CCCAAAGCAT TGGGAGTATA GGTGTGAGCC ACTATAACCG TCCTCACATC	300
ATATTTCTAA TCCCGAGACT GTAGAGCTGG TGTCTCTTT TCTAAAGGAT GTCAGTAGAG	360
AAGTGGAGTT CCCCAAAATT ACAGTTTCAC GTATTAGTCA AGTTTCTAAA ATACAGTAAT	420
AATGTTGAGA GCTGACATAG GGACTAACTT GGTTTTTTT TTTTTTTTT TTTTTCAAAT	480
TCTCACTGAA CTTTGATTTT GCTAAATAAG GACATTAAAA AAAAAACCAA AAAACTCCAC	540
TATTGCCTAT TGCCACTATT TGATTTTTA AAAAAATAAGC GTATTITAGC ATCTAAAAGT	600
AGGAAGGACC TCAAATAAAT GAGTCTTGT TCTTGGCCAG GGAAAACAGC GTTGTCAAGA	660
TTTGATAACT GTTTTCTAG GGTATGTGCT GTTATTCACT TAAAACCTTG CCTGGGACGC	720
TAGCATTCAAG TAAATACCTG TTGAATAAGC AAATGAAACT TAAGCTTCTA TGTATAGAAA	780
CCTAAGTCAC TTCACATTCT GATTAGCAGA GTAATTGAAT ATTCTTTCA ATGTGTAGCT	840
CTATCCCCAG AACCAACAGAA TATTGGAACT GTAAAGGCCA TCCTATAGTT TAACCAACTG	900
CGTTAAATAG ATAATAGAAA GATGTGGTAT GTGGCAGTGA CAACTGAAG GTTGTGACTA	960
GAACTCGGGT CTCTGGAGTG TTCTATTATA TCACACCAAG CTGGTCACCA GCCCATGTGT	1020
TGATCCTCCA TTGTGATAGC AACAAAGAAA AGACTTCAGG ACATTCTTC CTTTACCTA	1080

ATCCTTGATC	TGCAGTCCTA	TTTAGAAAAG	CTTAATGTTA	AAGATCTAGT	TTATTCAAAA	1140
CTAAAGATAA	CAAGGAGTAT	GAGAATTCT	ATTCGGAGT	GTAAAGGAGG	AGATGTTCC	1200
TTGGCTTCTC	TGAGCCTGCA	GGCCTTCCTT	GCTCTTAAG	GAAGTAGAGA	GAGGGAGGAA	1260
AGTAAAGTAT	GCTTTGTTT	TTAAGGTTA	CTTGCTGGG	AGTAGTTGC	ATGCCTTTG	1320
GTGTTCTGG	GTGGAATTAA	CTGACTTAAG	TTTAAGTAG	TTGGGACTAT	TTAAAAACAA	1380
TGCCTATCCA	ATGTTGCCA	TAAAGGCAGA	GGGTATTGGC	TTTAGAAGTT	AATTCTTCTC	1440
CAGGAGTGAA	AATTAGCTTC	TAAACCAGAA	GCAGCAGAGC	TAAATAAAGT	AATTTTCCAC	1500
CTGGCCAGTG	CATGATGTGA	AAGGTAGATT	AAAAAAATGA	GAGGGCCAT	TTCTGTATGA	1560
AAGACTAAGC	CATGTTGAAA	CAGCCCTGTT	GAGGATTTA	TTTTAAATCT	ATACATTCAC	1620
AAAGGAGCTT	TGTGTATGTC	TTTCCCTATT	TGTTGTTGG	ACTAGGAAGC	CCCACCCAGT	1680
GCTTGTGAA	GGCAGAAAGT	CGTTGAAAGC	AAGCTGGAT	TTGAACAGTG	GATTGAGGTT	1740
TCGAATATCC	AGTGAACCAA	AATATATCAG	GGTCCCCCTG	GCCAAGATGA	GTGACCATT	1800
TGAGGTGTTA	AGTATTCTT	GAATGGGAT	TTAGGAAAAA	TTTCTGTAT	TTCTGTGCTC	1860
ATTTTGTGA	CCTCTGTATG	TGCAAATCT	CTAAGGGGGT	TTTGCGCAC	TTAGATTCT	1920
TGGATGCAGA	TTGTTTGTA	TATGAAACAA	ATTTAAATT	TTTTGTATA	CACTGGATT	1980
AAAATAGTTT	ACTAAAGTGT	TTAATTCTT	TCATCTTAAT	TTTCACAGTT	CTTATAGTCT	2040
TTAGATTTAG	GGAGGCTGTT	GATGGCATCC	ACATGTGCAT	TTTAGTGGCA	TTAAAATGT	2100
ATTCAGCTGA	ATTTAACAAAT	TTCTGACCTA	AAACTGACA	TTTTAGATT	AAGTCGGTAA	2160
AGCACTGATT	TAAACTGGAT	TTTAACCTGGA	TGAAATTCTG	ATTTAATAAG	TGTACTGACT	2220
GGATAAAATG	CCAATGATT	AATTAACAAG	CACGTTAAC	AGGATGCCCT	ATATATTAGT	2280
TAAAAGTGA	GCAATTGAAT	TAGGTACCTT	CTCTGCTGCG	TGGAAAAGAC	CGTATGACTC	2340
ACCCACACCA	GCCTTCTCTT	CGCTCTGAGT	GTAGCTAAC	TTTCTGTGTT	TTTTCTCT	2400
AGGGTTGGA	AATCCCTGT	CTCCAGGTTG	CTGGGATTGA	CTTCTGCTC	AATTGAAACA	2460
CTCATTCAAT	GGAGACAAAG	AGAACTAATG	CTTGTGCTG	ATTCAATT	GAATCGAGGC	2520
ATTGGGAACC	CTGTATGCCT	TGTTGTTGGA	AAGAACCAAGT	GACACCATCA	CTGAGCTTCC	2580
TAAAAGTCG	AAGAAGTTAG	AGGACTATAC	ACTTCTTTT	GAACCTTTAT	AATAAATATT	2640
TGCTCTGGTT	TTTGGAACCC	AGGGCTGTTA	GAGGGTGAG	TGACAAGTCT	TACAAGTGGC	2700
CTTATTCCAA	CTCCAGAAAT	TGCCAACCG	AACTTGAGA	TTATATGAA	TCGAAAGTGA	2760
CAGGAAACAT	GCCAACCAA	TCCCTCTTAA	TGTACATGGA	TGGGCCAGAA	GTGATTGGCA	2820
GCTCTCTGG	CAGTCCGATG	GAGATGGAGG	ATGCCCTGTC	AATGAAAGGG	ACCGCTGTTG	2880
TTCCATTCCG	AGCTACACAA	GAAAAAAATG	TCATCCAAAT	CGAGGGTAT	ATGCCCTTGG	2940
ATTGCATGTT	CTGCAGCCAG	ACCTTCACAC	ATTCAAGAAGA	CCTTAATAAA	CATGTCTTAA	3000
TGCAACACCG	GCCTACCCCTC	TGTGAACCAAG	CAGTTCTTCG	GGTTGAAGCA	GAGTATCTCA	3060
GTCCGCTTGA	TTAAAGTCAA	GTGCGAACAG	AACCTCCCAA	GGAAAAGAAT	TGCAAGGAAA	3120

ATGAATTTAG	CTGTGAGGTA	TGTGGGCAGA	CATTTAGAGT	CGCTTTGAT	GTTGAGATCC	3180
ACATGAGAAC	ACACAAAGAT	TCTTCACTT	ACGGGTGTA	CATGTGCGGA	AGAAGATTCA	3240
AGGAGCCTTG	GTTCCTTAAA	AATCACATGC	GGACACATAA	TGGCAAATCG	GGGGCCAGAA	3300
GCAAACGTCA	GCAAGGCTTG	GAGAGTAGTC	CAGCAACGAT	CAACGAGGTC	GTCCAGGTGC	3360
ACGCAGGCCA	GAGCATCTCC	TCTCCTTACA	AAATCTGCAT	GGTTTGTGGC	TTCCTATTTC	3420
CAAATAAAGA	AAGTCTAATT	GAGCACCGCA	AGGTGCACAC	CAAAAAAAACT	GCTTTCGGTA	3480
CCAGCAGCGC	GCAGACAGAC	TCTCCACAAG	GAGGAATGCC	GTCCTCGAGG	GAGGACTTCC	3540
TGCAGTTGTT	CAACTTGAGA	CCAAAATCTC	ACCCTGAAAC	GGGGAAGAAG	CCTGTCAGAT	3600
GCATCCCTCA	GCTCGATCCG	TTCACCACCT	TCCAGGCTTG	GCAGCTGGCT	ACCAAAGGAA	3660
AAGTTGCCAT	TTGCCAAGAA	GTGAAGGAAT	CGGGGCAAGA	AGGGAGCACC	GACAACGACG	3720
ATTCGAGTTC	CGAGAAGGAG	CTTGGAGAAA	CAAATAAGGG	CAGTTGTGCA	GGCCTCTCGC	3780
AAGAGAAAGA	GAAGTGCAAA	CACTCCCACG	GCGAAGCGCC	CTCCGTGGAC	GCGGATCCCC	3840
AGTTACCCAG	TAGCAAGGAG	AAGCCCACTC	ACTGCTCCGA	GTGCGGCAAA	GCTTTCAGAA	3900
CCTACCACCA	GCTGGTCTTG	CACTCCAGGG	TCCACAAGAA	GGACCGGAGG	GCCGGCGCGG	3960
AGTCGCCAC	CATGTCTGTG	GACGGGAGGC	AGCCGGGGAC	GTGTTCTCCT	GACCTCGCCG	4020
CCCCTCTGGA	TGAAAATGGA	GCCGTGGATC	GAGGGGAAGG	TGGTTCTGAA	GACGGATCTG	4080
AGGATGGGCT	TCCCGAAGGA	ATCCATCTGG	GTAAGCTGCC	CTGTCTCCGT	CCCGTGTGT	4140
TCCGCCTGTG	TCTGTCTGTC	TCCCCGTCTC	CCCCCTCTA	TTCCCATCTC	CAGACAACGC	4200
TGGCCAGGAA	TGGGTTTGG	AGAGCCAGAG	TCAAGTCCAG	GCTCTTTTG	GTATCACTCT	4260
GTGTAAGTCA	TTAACCTCT	CAGGGCCTTA	ATTTTCTCAT	TTCTGTAATA	ACAGGGTTGA	4320
GTAAAGAGGT	CTCCTTGTTC	TGAAAATATA	TATATATTTT	TTAAACGTGT	ATCGTTTGC	4380
TCACAAAACA	CACTTTAAAA	AAAAAATAAC	TTGTGCATCC	AGCCCAAATG	CACTGCTTCT	4440
TAACTGGGGC	GATTTGTTC	CCAATCAGTA	TCTGGCAATG	TCTGGAGGCA	TTTTGGTTGT	4500
CATACTGTGT	GTGTGGGTGT	GCCTGCTGGC	ATCCAGTGGG	CAGAGGCCAG	GGACACTGCT	4560
CAGCATGGTA	CAGTGCACAG	GACAGCCCCA	TCATCAAAGA	ATTATCTGGT	CCCAAATGTC	4620
AATAGTTGA	GCATTGAGAG	ACCCTAGCCT	TCACTTAAGT	TTTCTGGCG	TTCCTGATCT	4680
TTTTCTGTAG	TGAATTCTA	GTGCCATAA	AAGGTACTGG	GAGTGATCAA	CTAGAGCCAG	4740
GAATATTATT	TGGGCAGCCG	TTTGGTGCTG	TCCAAAACCT	TGTCCTTCT	GTCTGGCAAG	4800
CTAGTATCCA	TTTATAGGTA	CCTCAGGAAC	CCAAATGATT	TGTCATAAAA	TACAAGGAAT	4860
GTGAGCACAC	TGAAGACATT	TTTAAGAAGG	CTCATTGCT	CAGCAGAATT	TTCAGTGTAC	4920
TAGTGGCATT	TATAGAAAGA	GAAGGTGATC	ACTGAAGGCA	TGCTCACATA	ATATTCTGA	4980
GCCCTGGTGG	GCGTTATCTA	GGGCAAAGGA	TTCCACCTGT	GTGGAGTT	GCGCCCATCC	5040
TCACTGTAGC	CAGAGCTTCT	CCTATCAGAG	TTTAGTATT	TGTTTGAATA	GAGGATCTT	5100
CTGCTTAAAAA	CAGTTGAAAAA	GACCCTGATG	GGCAGGCCGT	AATTGACAAG	CGAATGATGG	5160

GAACATGAAT CGGTCTTAGG GAAGCATCTG TCAAAGTGGT CCTTGGTTAA AACAAAGTGCC	5220
TCCTCCCTCTC AGTGTCACTT GATTGTGTGC TTGAATTCTT CGGAAAACGT GGTGTATGAG	5280
ACCCACGATG AATTGCCCCA CACGATTGAT TGGACTCTTC CTTCACCTGC TCTTCAGCCA	5340
GTGCCAGTTC CTTTCTGAT CATGTGATTG ACGTGAGAAC TGTAGTCTGT ATATCAAATC	5400
TTTAGAATGT TTTTGAGTTT CCTGGGACAC AGGAAACCCA GCACTTAGCA TACTACAAAT	5460
CTAATGTCTT AATGGCATCA TAAAAAGAGG CTTAAACAC AGACTCCAGT TAGCTAAGTG	5520
GTTTCTGCTA GTGCCGGTAC TGTTGCAGGG GCCCTGTGAG ATGCCCGAGT TCCCTGAAAG	5580
AAATGAAAAG GCCAGTTACC GGTAGGTGGT GTGGAAAACA TGGGCTAGAT CATCAGGCAG	5640
GACAGAATGC CTGGCTGTGG GTGGGAGCAC CCCAGCTTGG CGTTGAGTTC TGGTTCTACC	5700
ACTGCGTTGT TTTGTGACCA ATTATGAGTT GCTTAACCTT TCTTTGCTAC TATTTCCCTG	5760
TTTGCAAAAT GGTCATTGA CCCCTGTCTT CCACCTCCCA AGGACAATT CAACAGCCTA	5820
TTTGTAAAAAA GATCACAGTC CTTTAAAAAA TATAACTGTA AAGTCAGAGG TGATGCTTGA	5880
AAGAGCAGGA ACCAGGTAGA TGTGGAAATG TCATGTCCTT TGTTCTAAAG AAAAGGCATT	5940
TCATAGCTTT TTGGATATGA CGCAACATAC CATAAATCCT GACACATAGT TGGGAGTCGG	6000
AAATTGCAAC AACGCCAGT TATAAACCCA GCTAGTTGG GTATGATTGT AAGAAAAAAA	6060
AGCTGGCCAT TCTGTATTTG GGGATTGAT TTTCTAAAC TTATATTATC TTAGTAGTCT	6120
AGATTTATCA TATTGTACTA TCATCCTGGC TTTTTTAAGA CTTAAGAAGA TCAAGTAAAT	6180
TTTTTTTCT TTCTTTAGAC ACTATATAGA TCATCAAGGG TGTCTGTCTT ACAGGTGGAT	6240
AGTGATATGA TCTACAGTGA GGGGACATT ATTAAAAC TAAACATTCA TGTGTTTG	6300
GGGTGGTATT TTAACGGCAG CACCTCTGAT TGTCTTTGG AGGGCTGGTG TGTGTTGAA	6360
GTTCTGTCCT CCTTCCAGTG GACTCTAACT TCTCCTGATG CACGTGAGAC ACATTGTCCT	6420
ATTGTCCTGC AGAAACTAAA GCCAACACT GTCATCTGGG GACAGGTTT CATTGTCAG	6480
ATCTCTTTCG CCCACATGAG TGTGTGGA CAATACAGCC TGCTTCCAA AACTTGCTA	6540
AATTTGACA GACTTCCCTA GGTGCTTGCC CAATGCCAGA CTTTCTTTTC TGTTGAAGAT	6600
TAAGTTGTGC TTGCTGCCCT CTAGTGGTCA GTTGTAAAT CCTAACCTTA AACGGCTTAT	6660
TTTCCCTG GTGGTTGGGA AGTTGACGGT TTGTAATTGG CTCATTTTC TAAATTATTC	6720
TGAAGAAGAT AATTTTCCC GCCAGTATGT ATGTCCACCT TCAGTTGCC AGATCCTGCC	6780
TGCTCAGAGA CACTGAGAAC CGGAAGCTGC CGGGCAATT CAGTCTATGA AATGATCTT	6840
CTTGTGATTA AGGCAAACGA AGAACTGAAT GTTTAATAGT GTACTCTGCT GTACCCAGAA	6900
AAAAACAAAA CAAATCATG TTATAACACT CTAAAACCTC AAACAAACCTC CAACAGCATT	6960
TGGTGTGTGT CTAGCCGTTT TGTTCTAACCG CGATGTTATA TAAAAGAATT TTTTCATGCT	7020
TTCCAAAAAT GTTTATGTCA AGAATATTAA AGTCAGCATG CCTTATTCAAG GTACTTCAGC	7080
TACCTTCTTA TATAAATATT TTTGTTTTTC CTTTAAGATA AAAATGATGA TGGAGGAAAA	7140
ATAAAACATC TTACATCTTC AAGAGAGTGT AGTTATTGTG GAAAGTTTTT CCGTTCAAAT	7200

TATTACCTCA ATATTCACT CAGAACGCAT ACAGGTAAAG AACTTTTATT TTTTTAACCA	7260
TGCATTAGTT AAATTATGTA GTTATCTAAT TTTTTGTTG TTGTTGTTCA GATACTCTGC	7320
CAGATCCTTG GACTAGCTTA AGGATAAAATA TGTAGCATGT TGATTGCAGT GGTTATTTTT	7380
ATTCTTTAG TGCCATTGTA ACTTGAGCCA TTGTTCTTAT TTGCAGTTCA TTTCTTTCT	7440
TTCTTTTTG TTTTTGAGA CGGAGTCTTG CTCTGTCACC TCGGCTGGAG TGCAGTGGTG	7500
CAATTCGGC TCACTGCAGC CTCCACCTCC CTGGTTCAAG CAATACTCCT GCCTCAGCCT	7560
CCCCAGTAGT TGGGATTACA GGTACCTGCC ACCACACCCG GCTAATTCT GTATTTTAG	7620
TAGAGATGGG GTTTCACCAT GCTGGCCAGG CTGGTTTCGA ACTCCTGACC TCAAGTGATC	7680
CGCTCACCTT GGCCTCCCAGT GTGTTGCC TCCCATAGTG CTGGGATTAC AGGCGTGAGC	7740
CACCGCGCCC GGACAAAGTT CATTGTTA GTTATGACT GCTATGTCCT GACTCTTATC	7800
TTATTAAAAG CTACAGTATT TTAAATGCT GCATCTTATG TCTTATGAT TGAGAATGAA	7860
ATGAGAATCT ATTTAGTAGT CTTGAGATTG TGAAAGGAGC TATGACATCA TGATGTAGGA	7920
GGCTGCGTAG ATTTGAAATT TCATCTCTTC CACTTACTAT CTGTGCACCC TTGGGCAAGT	7980
TATTTAACCT TTTTGTGCTT TTAGTTTCT TTGCTGTAAA AGTAGAATAA TACATATTTC	8040
CCTAGGGCTG TTAGGAAGAT TAAATAAGTT AGAAGTGTG CTGTTAATT TTCTATTGAA	8100
GATAGGCATT CATAATTCA AATATTCAATT ACAGTAAGGA TGATAAAAGAA CTGATGAGAA	8160
ATCCTATGTG ATAGTAGATC GAGAAAGCAA AAGGAGGAAA GAAGCCTGTT TTCTTAATAA	8220
ATAGATATTGATCTT GATCTATTTC AGTGCTTTTC ATACACTTCT ATAATAAAAGT GCCATTCTT	8280
GCCTTAGGTG AAAAACATA CAAATGTGAA TTTTGTGAAT ATGCTGCAGC CCAGAAGACA	8340
TCTCTGAGGT ATCACTTGGA GAGACATCAC AAGGAAAAAC AAACCGATGT TGCTGCTGAA	8400
GTCAAGAACG ATGGTAAAAA TCAGGACACT GAAGATGCAC TATTAACCGC TGACAGTGCG	8460
CAAACAAAAA ATTTGAAAAG ATTTTTGAT GGTGCCAAAG ATGTTACAGG CAGTCCACCT	8520
GCAAAGCAGC TTAAGGAGAT GCCTCTGTT TTTCAGAATG TTCTGGCAG CGCTGTCCCTC	8580
TCACCAGCAC ACAAAAGATAC TCAGGATTTC CATAAAAATG CAGCTGATGA CAGTGCTGAT	8640
AAAGTGAATA AAAACCTAC CCCTGCTTAC CTGGACCTGT TAAAAAAGAG ATCAGCAGTT	8700
GAAACTCAGG CAAATAACCT CATCTGTAGA ACCAAGGCAG ATGTTACTCC TCCTCCGGAT	8760
GGCAGTACCA CCCATAACCT TGAAGTTAGC CCCAAAGAGA AGCAAACGGA GACCGCAGCT	8820
GACTGCAGAT ACAGGCCAAG TGTGGATTGT CACGAAAAAC CTTTAAATTG ATCCGTGGGG	8880
GCTCTTCACA ATTGCCCCGC AATTCTTTG AGTAAAAGTT TGATTCCAAG TATCACCTGT	8940
CCATTTGTA CCTTCAAGAC ATTTTATCCA GAAGTTTAA TGATGCACCA GAGACTGGAG	9000
CATAAAATACA ATCCTGACGT TCATAAAAAC TGTCGAAACA AGTCCTTGCT TAGAAGTCGA	9060
CGTACCGGAT GCCCGCCAGC GTTGCTGGGA AAAGATGTGC CTCCCCCTCCC TAGTTCTGT	9120
AAACCCAAGC CCAAGTCTGC TTTCCCGGCG CAGTCCAAAT CCCTGCCATC TGCGAAGGGG	9180
AAGCAGAGCC CTCCTGGGCC AGGCAAGGCC CCTCTGACTT CAGGGATAGA CTCTAGCACT	9240

TTAGCCCCAA	GTAACCTGAA	GTCCCACAGA	CCACAGCAGA	ATGTGGGGGT	CCAAGGGGCC	9300
GCCACCAGGC	AACAGCAATC	TGAGATGTTT	CCTAAAACCA	GTGTTCCCC	TGCACCGGAT	9360
AAGACAAAAA	GACCGAGAC	AAAATTGAAA	CCTCTTCCAG	TAGCTCCTTC	TCAGCCCACC	9420
CTCGGCAGCA	GTAACATCAA	TGGTTCCATC	GACTACCCCG	CCAAGAACGA	CAGCCCGTGG	9480
GCACCTCCGG	GAAGAGACTA	TTTCTGTAAT	CGGAGTGCCA	GCAATACTGC	AGCAGAATT	9540
GGTGAGCCCC	TTCCAAAAAG	ACTGAAGTCC	AGCGTGGTTG	CCCTTGACGT	TGACCAGCCC	9600
GGGGCCAATT	ACAGAACAGG	CTATGACCTT	CCCAAGTACC	ATATGGTCAG	AGGCATCACA	9660
TCACTGTTAC	CGCAGGACTG	TGTGTATCCG	TCGCAGGC	TGCCTCCAA	ACCAAGGTT	9720
CTGAGCTCCA	GCGAGGTCGA	TTCTCCAAAT	GTGCTGACTG	TTCAGAACCC	CTATGGTGGC	9780
TCCGGGCCAC	TTTACACTTG	TGTGCCTGCT	GGTAGTCCAG	CATCCAGCTC	GACGTTAGAA	9840
GGTATTGCAT	GAGGGCGTC	GTGTTAAAT	GGCTGCCTAC	AGTGATTAAT	AGCTAATCCA	9900
GGCATTCTCA	GTGGAGATGG	TACCACTCCC	AAGGGTGGGG	GGTAGGCAGC	CAGAACGTT	9960
TGGGGTCAC	AGAGAGAAC	ATTCTTAGAT	ACGGCAGTGG	TTTGTGGTCC	TCCAAGGCTT	10020
ACTTAACTCT	GTGGGTTAA	CTCTTAACCC	TGTGTATTTT	ATTCTTTGA	TTTGTGTTAGT	10080
CTTACTTTAT	TTTAGAGAA	AGGGTCTTGC	TCCGTCATCT	AGATTGGAGT	GCAGCGGTGT	10140
AATCATAGCT	TACTGTAGTC	TTGAATTCC	GAGTTCAAGA	GATCCTCTG	CCTCAGCTTC	10200
CCAGGTAGCT	GAGACTATAT	GTGCTGCTAC	CATGCACAGC	TGATTTTAA	ATTTTTTTG	10260
TAGAGATGGA	GTTGCCAGG	CTGGTCTTGA	ACTCCTGGCC	TGAGGTGATC	CTCCTGCGTT	10320
GACCTCCAA	GTATCTTAGA	CTACAGATGC	ACTCCACCAC	GCTTG		10365

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3186 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..3186
- (D) OTHER INFORMATION: /note= "ZABC1 Open Reading Frame"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATGCAATCGA	AAGTGACAGG	AAACATGCCA	ACTCAATCCC	TCTTAATGTA	CATGGATGGG	60
CCAGAAGTGA	TTGGCAGCTC	TCTTGGCAGT	CCGATGGAGA	TGGAGGATGC	CTTGTCAATG	120
AAAGGGACCG	CTGTTGTTCC	ATTCCGAGCT	ACACAAGAAA	AAAATGTCAT	CCAAATCGAG	180
GGGTATATGC	CCTTGGATTG	CATGTTCTGC	AGCCAGACCT	TCACACATTC	AGAAGACCTT	240
AATAAACATG	TCTTAATGCA	ACACCGGCT	ACCCCTGTG	AACCAGCAGT	TCTTCGGGTT	300

GAAGCAGAGT ATCTCAGTCC GCTTGATAAA AGTCAGTGC GAACAGAACCC TCCCAAGGAA	360
AAGAATTGCA AGGAAAATGA ATTTAGCTGT GAGGTATGTG GGCAGACATT TAGAGTCGCT	420
TTTGATGTTG AGATCCACAT GAGAACACAC AAAGATTCTT TCACTTACGG GTGTAACATG	480
TGCGGAAGAA GMITSRRSSA GCCTTGGTTT CTTAAAAATC ACATGCGGAC ACATAATGGC	540
AAATCGGGGG CCAGAAGCAA ACTGCAGCAA GGCTTGGAGA GTAGTCCAGC AACGATCAAC	600
GAGGTCGTCC AGGTGCACGC GGCGAGAGC ATCTCCTCTC CTTACAAAAT CTGCATGGTT	660
TGTGGCTTCC TATTTCAAA TAAAGAAAGT CTAATTGAGC ACCGCAAGGT GCACACCAAA	720
AAAACGTCTT TCGGTACCAAG CAGCGCGAG ACAGACTCTC CACAAGGAGG AATGCCGTCC	780
TCGAGGGAGG ACTTCCTGCA GTTGTCAAC TTGAGACCAA AATCTCACCC TGAAACGGGG	840
AAGAAGCCTG TCAGATGCAT CCCTCAGCTC GATCCGTTCA CCACCTTCCA GGCTTGGCAG	900
CTGGCTACCA AAGGAAAAGT TGCCATTTGC CAAGAAGTGA AGGAATCGGG GCAAGAAGGG	960
AGCACCGACA ACGACGATTC GAGTCCGAG AAGGAGCTTG GAGAAACAAA TAAGGGCAGT	1020
TGTGCAGGCC TCTCGCAAGA GAAAGAGAAG TGCAAACACT CCCACGGCGA AGGCCCTCC	1080
GTGGACGCGG ATCCCAAGTT ACCCAGTAGC AAGGAGAAGC CCACTCACTG CTCCGAGTGC	1140
GGCAAAGCTT TCAGAACCTA CCACCAGCTG GTCTTGCCT CCAGGGTCCA CAAGAAGGAC	1200
CGGAGGGCCG GCGCGGAGTC GCCCACCATG TCTGTGGACG GGAGGCAGCC GGGGACGTGT	1260
TCTCCTGACC TCGCCGCCCTC TCTGGATGAA AATGGAGCCG TGGATCGAGG GGAAGGTGGT	1320
TCTGAAGACG GATCTGAGGA TGGGCTTCCC GAAGGAATCC ATCTGGATAA AAATGATGAT	1380
GGAGGAAAAAA TAAAACATCT TACATCTTCA AGAGAGTGT GTTATTGTGG AAAGTTTTTC	1440
CGTTCAAATT ATTACCTCAA TATTCTCTC AGAACGCATA CAGGTGAAAA ACCATACAAA	1500
TGTGAATTGT GTGAATATGC TGCAGCCCAG AAGACATCTC TGAGGTATCA CTTGGAGAGA	1560
CATCACAAGG AAAAACAAAC CGATGTTGCT GCTGAAGTCA AGAACGATGG TAAAATCAG	1620
GACACTGAAG ATGCACTATT AACCGCTGAC AGTGCAGAAA CCAAAATTT GAAAAGATT	1680
TTTGATGGTG CCAAAGATGT TACAGGCAGT CCACCTGCAA AGCAGCTTAA GGAGATGCCT	1740
TCTGTTTTTC AGAATGTTCT GGGCAGCGCT GTCTCTCAC CAGCACACAA AGATACTCAG	1800
GATTTCCATA AAAATGCAGC TGATGACAGT GCTGATAAAG TGAATAAAAAA CCCTACCCCT	1860
GCTTACCTGG ACCTGTTAAA AAAGAGATCA GCAGTTGAAA CTCAGGCAA TAACCTCATC	1920
TGTAGAACCA AGGCAGATGT TACTCCTCCT CCGGATGGCA GTACCACCCA TAACCTTGAA	1980
GTTAGCCCCA AAGAGAAGCA AACGGAGACC GCAGCTGACT GCAGATACAG GCCAAGTGTG	2040
GATTGTCACG AAAAACCTTT AAATTTATCC GTGGGGGCTC TTCACAATTG CCCGGCAATT	2100
TCTTGAGTA AAAGTTGAT TCCAAGTATC ACCTGTCCAT TTTGTACCTT CAAGACATT	2160
TATCCAGAAG TTTAATGAT GCACCAAGAGA CTGGAGCATA AATACAATCC TGACGTTCAT	2220
AAAAACTGTC GAAACAAGTC CTTGCTTAGA AGTCGACGTA CGGGATGCCGCC GCGAGCGTTG	2280
CTGGGAAAAG ATGTGCCTCC CCTCTCTAGT TTCTGTAAAC CCAAGCCCAA GTCTGTTTC	2340

CCGGCGCAGT CCAAATCCCT GCCATCTGCG AAGGGGAAGC AGAGCCCTCC TGGGCCAGGC	2400
AAGGCCCTC TGACTTCAGG GATAGACTCT AGCACTTTAG CCCCAAGTAA CCTGAAGTCC	2460
CACAGACCAC AGCAGAATGT GGGGGTCCAA GGGGCCGCCA CCAGGCAACA GCAATCTGAG	2520
ATGTTTCCTA AAACCAGTGT TTCCCCTGCA CCGGATAAGA CAAAAAGACC CGAGACAAAAA	2580
TTGAAACCTC TTCCAGTAGC TCCTTCTCAG CCCACCCCTCG GCAGCAGTAA CATCAATGGT	2640
TCCATCGACT ACCCCGCCAA GAACGACAGC CCGTGGCAC CTCCGGGAAG AGACTATTTC	2700
TGTAATCGGA GTGCCAGCAA TACTGCAGCA GAATTTGGTG AGCCCCCTCC AAAAAGACTG	2760
AAGTCCAGCG TGGTTGCCCT TGACGTTGAC CAGCCCCGGG CCAATTACAG AAGAGGCTAT	2820
GACCTTCCCA AGTACCATAT GGTCAGAGGC ATCACATCAC TGTTACCGCA GGACTGTGTG	2880
TATCCGTCGC AGGCCGCTGCC TCCCAAACCA AGGTTCTGA GCTCCAGCGA GGTGATTCT	2940
CCAAATGTGC TGACTGTTCA GAAGCCCTAT GGTGGCTCCG GGCCACTTTA CACTTGTGTG	3000
CCTGCTGGTA GTCCAGCATC CAGCTCGACG TTAGAAGGTC TTGGTGGATG TCAGTGCTTA	3060
CTCCCCATGA AATTAAATTT TACTTCATCC TTTGAGAAGC GAATGGTGAA AGCTACTGAA	3120
ATAAGCTGTG ATTGTACTGT ACATAAAACA TATGAGGAAT CTGCAAGGAA CACTACAGTT	3180
GTGTAA	3186

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1061 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1061
- (D) OTHER INFORMATION: /note= "ZABC1 Protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Gln Ser Lys Val Thr Gly Asn Met Pro Thr Gln Ser Leu Leu Met			
1	5	10	15
Tyr Met Asp Gly Pro Glu Val Ile Gly Ser Ser Leu Gly Ser Pro Met			
20	25	30	
Glu Met Glu Asp Ala Leu Ser Met Lys Gly Thr Ala Val Val Pro Phe			
35	40	45	
Arg Ala Thr Gln Glu Lys Asn Val Ile Gln Ile Glu Gly Tyr Met Pro			
50	55	60	
Leu Asp Cys Met Phe Cys Ser Gln Thr Phe Thr His Ser Glu Asp Leu			
65	70	75	80
Asn Lys His Val Leu Met Gln His Arg Pro Thr Leu Cys Glu Pro Ala			
85	90	95	

Val Leu Arg Val Glu Ala Glu Tyr Leu Ser Pro Leu Asp Lys Ser Gln
 100 105 110
 Val Arg Thr Glu Pro Pro Lys Glu Lys Asn Cys Lys Glu Asn Glu Phe
 115 120 125
 Ser Cys Glu Val Cys Gly Gln Thr Phe Arg Val Ala Phe Asp Val Glu
 130 135 140
 Ile His Met Arg Thr His Lys Asp Ser Phe Thr Tyr Gly Cys Asn Met
 145 150 155 160
 Cys Gly Arg Xaa Xaa Xaa Xaa Pro Trp Phe Leu Lys Asn His Met Arg
 165 170 175
 Thr His Asn Gly Lys Ser Gly Ala Arg Ser Lys Leu Gln Gln Gly Leu
 180 185 190
 Glu Ser Ser Pro Ala Thr Ile Asn Glu Val Val Gln Val His Ala Ala
 195 200 205
 Glu Ser Ile Ser Ser Pro Tyr Lys Ile Cys Met Val Cys Gly Phe Leu
 210 215 220
 Phe Pro Asn Lys Glu Ser Leu Ile Glu His Arg Lys Val His Thr Lys
 225 230 235 240
 Lys Thr Ala Phe Gly Thr Ser Ser Ala Gln Thr Asp Ser Pro Gln Gly
 245 250 255
 Gly Met Pro Ser Ser Arg Glu Asp Phe Leu Gln Leu Phe Asn Leu Arg
 260 265 270
 Pro Lys Ser His Pro Glu Thr Gly Lys Lys Pro Val Arg Cys Ile Pro
 275 280 285
 Gln Leu Asp Pro Phe Thr Thr Phe Gln Ala Trp Gln Leu Ala Thr Lys
 290 295 300
 Gly Lys Val Ala Ile Cys Gln Glu Val Lys Glu Ser Gly Gln Glu Gly
 305 310 315 320
 Ser Thr Asp Asn Asp Asp Ser Ser Glu Lys Glu Leu Gly Glu Thr
 325 330 335
 Asn Lys Gly Ser Cys Ala Gly Leu Ser Gln Glu Lys Glu Lys Cys Lys
 340 345 350
 His Ser His Gly Glu Ala Pro Ser Val Asp Ala Asp Pro Lys Leu Pro
 355 360 365
 Ser Ser Lys Glu Lys Pro Thr His Cys Ser Glu Cys Gly Lys Ala Phe
 370 375 380
 Arg Thr Tyr His Gln Leu Val Leu His Ser Arg Val His Lys Lys Asp
 385 390 395 400
 Arg Arg Ala Gly Ala Glu Ser Pro Thr Met Ser Val Asp Gly Arg Gln
 405 410 415
 Pro Gly Thr Cys Ser Pro Asp Leu Ala Ala Pro Leu Asp Glu Asn Gly
 420 425 430
 Ala Val Asp Arg Gly Glu Gly Ser Glu Asp Gly Ser Glu Asp Gly
 435 440 445

Leu Pro Glu Gly Ile His Leu Asp Lys Asn Asp Asp Gly Gly Lys Ile
 450 455 460
 Lys His Leu Thr Ser Ser Arg Glu Cys Ser Tyr Cys Gly Lys Phe Phe
 465 470 475 480
 Arg Ser Asn Tyr Tyr Leu Asn Ile His Leu Arg Thr His Thr Gly Glu
 485 490 495
 Lys Pro Tyr Lys Cys Glu Phe Cys Glu Tyr Ala Ala Ala Gln Lys Thr
 500 505 510
 Ser Leu Arg Tyr His Leu Glu Arg His His Lys Glu Lys Gln Thr Asp
 515 520 525
 Val Ala Ala Glu Val Lys Asn Asp Gly Lys Asn Gln Asp Thr Glu Asp
 530 535 540
 Ala Leu Leu Thr Ala Asp Ser Ala Gln Thr Lys Asn Leu Lys Arg Phe
 545 550 555 560
 Phe Asp Gly Ala Lys Asp Val Thr Gly Ser Pro Pro Ala Lys Gln Leu
 565 570 575
 Lys Glu Met Pro Ser Val Phe Gln Asn Val Leu Gly Ser Ala Val Leu
 580 585 590
 Ser Pro Ala His Lys Asp Thr Gln Asp Phe His Lys Asn Ala Ala Asp
 595 600 605
 Asp Ser Ala Asp Lys Val Asn Lys Asn Pro Thr Pro Ala Tyr Leu Asp
 610 615 620
 Leu Leu Lys Lys Arg Ser Ala Val Glu Thr Gln Ala Asn Asn Leu Ile
 625 630 635 640
 Cys Arg Thr Lys Ala Asp Val Thr Pro Pro Pro Asp Gly Ser Thr Thr
 645 650 655
 His Asn Leu Glu Val Ser Pro Lys Glu Lys Gln Thr Glu Thr Ala Ala
 660 665 670
 Asp Cys Arg Tyr Arg Pro Ser Val Asp Cys His Glu Lys Pro Leu Asn
 675 680 685
 Leu Ser Val Gly Ala Leu His Asn Cys Pro Ala Ile Ser Leu Ser Lys
 690 695 700
 Ser Leu Ile Pro Ser Ile Thr Cys Pro Phe Cys Thr Phe Lys Thr Phe
 705 710 715 720
 Tyr Pro Glu Val Leu Met Met His Gln Arg Leu Glu His Lys Tyr Asn
 725 730 735
 Pro Asp Val His Lys Asn Cys Arg Asn Lys Ser Leu Leu Arg Ser Arg
 740 745 750
 Arg Thr Gly Cys Pro Pro Ala Leu Leu Gly Lys Asp Val Pro Pro Leu
 755 760 765
 Ser Ser Phe Cys Lys Pro Lys Pro Lys Ser Ala Phe Pro Ala Gln Ser
 770 775 780
 Lys Ser Leu Pro Ser Ala Lys Gly Lys Gln Ser Pro Pro Gly Pro Gly
 785 790 795 800

Lys Ala Pro Leu Thr Ser Gly Ile Asp Ser Ser Thr Leu Ala Pro Ser
 805 810 815
 Asn Leu Lys Ser His Arg Pro Gln Gln Asn Val Gly Val Gln Gly Ala
 820 825 830
 Ala Thr Arg Gln Gln Gln Ser Glu Met Phe Pro Lys Thr Ser Val Ser
 835 840 845
 Pro Ala Pro Asp Lys Thr Lys Arg Pro Glu Thr Lys Leu Lys Pro Leu
 850 855 860
 Pro Val Ala Pro Ser Gln Pro Thr Leu Gly Ser Ser Asn Ile Asn Gly
 865 870 875 880
 Ser Ile Asp Tyr Pro Ala Lys Asn Asp Ser Pro Trp Ala Pro Pro Gly
 885 890 895
 Arg Asp Tyr Phe Cys Asn Arg Ser Ala Ser Asn Thr Ala Ala Glu Phe
 900 905 910
 Gly Glu Pro Leu Pro Lys Arg Leu Lys Ser Ser Val Val Ala Leu Asp
 915 920 925
 Val Asp Gln Pro Gly Ala Asn Tyr Arg Arg Gly Tyr Asp Leu Pro Lys
 930 935 940
 Tyr His Met Val Arg Gly Ile Thr Ser Leu Leu Pro Gln Asp Cys Val
 945 950 955 960
 Tyr Pro Ser Gln Ala Leu Pro Pro Lys Pro Arg Phe Leu Ser Ser Ser
 965 970 975
 Glu Val Asp Ser Pro Asn Val Leu Thr Val Gln Lys Pro Tyr Gly Gly
 980 985 990
 Ser Gly Pro Leu Tyr Thr Cys Val Pro Ala Gly Ser Pro Ala Ser Ser
 995 1000 1005
 Ser Thr Leu Glu Gly Leu Gly Cys Gln Cys Leu Leu Pro Met Lys
 1010 1015 1020
 Leu Asn Phe Thr Ser Ser Phe Glu Lys Arg Met Val Lys Ala Thr Glu
 1025 1030 1035 1040
 Ile Ser Cys Asp Cys Thr Val His Lys Thr Tyr Glu Glu Ser Ala Arg
 1045 1050 1055
 Asn Thr Thr Val Val
 1060

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3066 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..3066
 - (D) OTHER INFORMATION: /note= "1b1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGAAACAGCT ATGACCATGA TTACGCCAAG CTCGAAATTA ACCCTCACTA AAGGGAACAA	60
AAGCTGGAGC TCCACCGCGG TGGCGGCCGC TCTAGAACTA GTGGATCCCC CGGGCTGCAG	120
GAATTCCGGCA CGAGGCTCCA CCGACAGCCA GGCACGGGC AGCACGCCTT GGAGACCCAG	180
GACCCCTGTGC AGGAGCAGCT CCGGGTGACA CGAGGGGACT GAAGATACTC CCACAGGGC	240
TCAGCAGGAG CAATGGGTAA CCAAATGAGT GTTCCCCAAA GAGTTGAAGA CCAAGAGAAT	300
GAACCAGAAG CAGAGACTTA CCAGGACAAC GCGTCTGCTC TGAACGGGGT TCCAGTGGTG	360
GTGTCGACCC ACACAGTTCA GCACTTAGAG GAAGTCGACT TGGGAATAAG TGTCAAGACG	420
GATAATGTGG CCACTTCTTC CCCCAGAGACA ACGGAGATAA GTGCTGTTGC GGATGCCAAC	480
GGAAAGAACAT TTGGGAAAGA GGCCAAACCC GAGGCACCAAG CTGCTAAATC TCGTTTTTC	540
TTGATGCTCT CTCGGCCTGT ACCAGGACGT ACCGGAGACC AAGCCGCAGA TTCATCCCTT	600
GGATCAGTGA AGCTTGATGT CAGCTCCAAT AAAGCTCCAG CGAACAAAGA CCCAAGTGAG	660
AGCTGGACAC TTCCGGTGGC AGCTGGACCG GGGCAGGACA CAGATAAAAC CCCAGGGCAC	720
GCCCCGGCCC AAGACAAGGT CCTCTCTGCC GCCAGGGATC CCACGCTTCT CCCACCTGAG	780
ACAGGGGGAG CAGGAGGAGA AGCTCCCTCC AAGCCCAAGG ACTCCAGCTT TTTTGACAAA	840
TTCTTCAAGC TGGACAAGGG ACAGGAAAAG GTGCCAGGTG ACAGCCAACA GGAAGCCAAG	900
AGGGCAGAGC ATCAAGACAA GGTGGATGAG GTTCCCTGGCT TATCAGGGCA GTCCGATGAT	960
GTCCCTGCAG GGAAGGACAT AGTTGACGGC AAGGAAAAAG AAGGACAAGA ACTTGGAACT	1020
GCGGATTGCT CTGTCCTGG GGACCCAGAA GGACTGGAGA CTGCAAAGGA CGATTCCCAG	1080
GCAGCAGCTA TAGCAGAGAA TAATAATTCC ATCATGAGTT TCTTTAAAC TCTGGTTCA	1140
CCTAACAAAG CTGAAACAAA AAAGGACCCA GAAGACACGG GTGCTGAAAA GTCACCCACC	1200
ACTTCAGCTG ACCTTAAGTC AGACAAAGCC AACTTTACAT CCCAGGAGAC CCAAGGGCT	1260
GGCAAGAATT CCAAAGGATG CAACCCATCG GGGCACACAC AGTCCGTGAC AACCCCTGAA	1320
CCTGCGAAGG AAGGCACCAA GGAGAAATCA GGACCCACCT CTCTGCCTCT GGGCAAACCTG	1380
TTTTGGAAAA AGTCAGTTAA AGAGGACTCA GTCCCCACAG GTGCGGAGGA GAATGTGGTG	1440
TGTGAGTCAC CAGTAGAGAT TATAAAGTCC AAGGAAGTAG AATCAGCCTT ACAAAACAGTG	1500
GACCTCAACG AAGGAGATGC TGCACCTGAA CCCACAGAAG CGAAACTCAA AAGAGAAGAA	1560
AGCAAACCAA GAACCTCTCT GATGGCGTTT CTCAGACAAA TGTCAGTGAA AGGGGATGGA	1620
GGGATCACCC ACTCAGAAGA AATAAAATGGG AAAGACTCCA GCTGCCAAC ACAGACTCC	1680
ACAGAAAAGA CTATCACACC GCCAGAGCCT GAACCAACAG GAGCACCACA GAAGGGTAA	1740
GAGGGCTCCT CGAAGGACAA GAAGTCAGCA GCCGAGATGA ACAAGCAGAA GAGCAACAAG	1800
CAGGAAGCCA AAGAACCCAGC CCAGTGCACA GAGCAGGCCA CGGTGGACAC GAACTCACTG	1860
CAGAATGGGG ACAAGCTCCA AAAGAGACCT GAGAAGCGGC AGCAGTCCCT TGGGGGCTTC	1920
TTTAAAGGCC TGGGACCAAA GCGGATGTTG GATGCTCAAG TGCAACAGA CCCAGTATCC	1980

ATCGGACCAG TTGGCAAACC CAAGTAAACA AATCAGCACG GTTCCCACCA GGTTCTCCTG	2040
CCACCAAGAT GTGTTCTCCT TACTCCATCT CCTCCCCAAA CACGCTCCAT GTATATATTTC	2100
TTCTGATGGC CAGCAAATGA AATTCTGCCT AGAAATTAAG CCCGAGCTGT TGTATATTGA	2160
GGTGTATTAT TTACGTCTCT GGTCCAGTCT TTTCTGGCAA ATAACAGTAA AGATGGTTA	2220
GCAGGTCACC TAGTTGGTC AGAAGAGTCG ATGATCACCA AGCAGGAAAG GGAGGGAATA	2280
GAGGAATGTG TTCGGGTTAA GTGATGAAAA TGGCAGTGGT GGCCGGCGT GGTGGCTCTC	2340
GCCTGTAATC TCAGCACTTT GGGAGGCCGA GGCAGGTGGA TCACCTGAGG TCAGGAGTTC	2400
AAGACTAGCC TGGCCAACAT CATGAAACCC CGTCTCTACT AAAAATACAA AAATTAGCCA	2460
GGCATGGTGG CACACACCTG TAGTCCCAGC TACTCGGGAG CCCAACGCAC GAGAACCGCT	2520
TGTACCCAGG AGGTGGAGGT TGCAGTGAGC CGAAGTTGCA CCATTGCACT CCACCCCTGGG	2580
CGACAGAGCA AGATTCTATC AAAAAAAA GGCAGTGGCA AGTAAGTTAT AGAAGAGAAA	2640
TGCTGCTAGA AGGAATTAAG CGTTGTAGTA AACCGTGTGCT CATCCTCTAA GCTTGAAGAA	2700
GGGAGACGAA AATCCATTG TTTAAATTCA CATCTCAAGG AGGGAGAACCGGGCTGTGT	2760
TGGGTGGTTG CCAATTCCCT AGAACGGAAT GTGTGGGTA TAGAAAAAGG AATGAATAAG	2820
CGTTGTTTT CAAATAGGGT CCTTGTAAGT TATTGATGAG AGGGAAAAGA TTGACTGGGG	2880
AGGGCTTAAA ATGATTGGG AAAACAATTG CTTTGAGGC TCAGTGACAA CGGCAAAGAT	2940
TACAACCTAA AAAAAAAA AAAAAAAACTC GAGACTAGTT CTCTCTCTCT CTCGTGCCGA	3000
ATTCGATATC AAGCTTATCG ATACCGTCGA CCTCGAGGGG GGGCCCGGTA CCCAATTGCGC	3060
CCTATA	3066

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TTGGCATTGG TATCAGGTAG CTG

23

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TTGGAGCAGA GAGGGGATTG TGTG

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AATCCCCTCA AACCCCTGCTG CTAC

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TGGAGCCTGA ACTTCTGCAA TC

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CCGGGATACC GACATTG

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TGCACATAAA ACAGCCAGC

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TTGGAATCAA TGGAGCAAAA

20

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

AGCTTTACCC AATGTGGTCC

20

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GTGGTGAACA CCAATAATG G

21

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AAGCAAATAA AACCAATAAA CTCG

24

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CAAGATCTGA CCCCGTCAAT C

21

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GACTTCTTCA GGAAAGAGAT CAGTG

25

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GCCATGTACC CACCTGAAAA ATC

23

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TCAGAACACC CGTGCAGAAT TAAG

24

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CCTAAAAACTT GGTGCTTAAA TCTA

24

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GTCTCACAAG GCAGATGTGG

20

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TTTGTGTATG TTGAGCCATC

20

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CTTCCAATCT CATTCTATGA GG

22

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GCTTGTAA GTGTCAGGG

22

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CACTCTGGTA AATGACCTTT GTC

23

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CCTACACCAT TCCAACTTTG G

21

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GCCAGATGTA TGTTGCTAC GGAAC

25

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

TCTCAAAACCT GTCCACTTCT TG

22

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CTGCTGTGGT GGAGAATGG

19

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

TGTCCTCCTT CTCCCTCATC CTAC

24

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

AATGCCTCCA CTCACAGGAA TG

22

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CCTCTTCAGT GTCTTCCTAT TGA

23

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GGGAGGAGGT TGTAGGCAAC

20

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

AGCAAAGCAA AGGTGGCACAC C

21

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

TGACATGGGA GAAGACACAC TTCC

24

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

AGGTTTACCA ATGTGTTTGG

20

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TCTACATCCC ATTCTCTTCT G